

OIPE

RAW SEQUENCE LISTING

DATE: 08/13/2001

PATENT APPLICATION: US/09/920,677

TIME: 11:07:29

Input Set : A:\RTS-0245 Sequence Listing.txt

Output Set: N:\CRF3\08132001\I920677.raw

Does Not Comply
Corrected Diskette Needed

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6 <110> APPLICANT: Brett P. Monia
7   Lex M. Cowsert
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION
11 <130> FILE REFERENCE: RTS-0245
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/920,677
C--> 13 <141> CURRENT FILING DATE: 2001-08-01
13 <160> NUMBER OF SEQ ID NOS: 49
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctctcaggg                                     20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga                                     20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2346
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <220> FEATURE:
50 <221> NAME/KEY: CDS
51 <222> LOCATION: (28)...(1605)
53 <400> SEQUENCE: 3
54 gcacgaggct gcggcgggtc cgggccc atg agg cga cga agg agg cgg gac ggc       54
55                               Met Arg Arg Arg Arg Arg Arg Arg Asp Gly
56                               1                               5
58 ttt tac cca gcc ccg gac ttc cga gac agg gaa gct gag gac atg gca       102
59 Phe Tyr Pro Ala Pro Asp Phe Arg Asp Arg Glu Ala Glu Asp Met Ala
60 10                               15                               20                               25
62 gga gtg ttt gac ata gac ctg gac cag cca gag gac gcg ggc tct gag       150
63 Gly Val Phe Asp Ile Asp Leu Asp Gln Pro Glu Asp Ala Gly Ser Glu
64                               30                               35                               40
66 gat gag ctg gag gag ggg ggt cag tta aat gaa agc atg gac cat ggg       198
67 Asp Glu Leu Glu Glu Gly Gly Gln Leu Asn Glu Ser Met Asp His Gly
68                               45                               50                               55
70 gga gtt gga cca tat gaa ctt ggc atg gaa cat tgt gag aaa ttt gaa       246
71 Gly Val Gly Pro Tyr Glu Leu Gly Met Glu His Cys Glu Lys Phe Glu
72                               60                               65                               70

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| | | |
|-----|---|------|
| 74 | atc tca gaa act agt gtg aac aga ggg cca gaa aaa atc aga cca gaa | 294 |
| 75 | Ile Ser Glu Thr Ser Val Asn Arg Gly Pro Glu Lys Ile Arg Pro Glu | |
| 76 | 75 80 85 | |
| 78 | tgt ttt gag cta ctt cgg gta ctt ggt aaa ggg ggc tat gga aag gtt | 342 |
| 79 | Cys Phe Glu Leu Leu Arg Val Leu Gly Lys Gly Gly Tyr Gly Lys Val | |
| 80 | 90 95 100 105 | |
| 82 | ttt caa gta cga aaa gta aca gga gca aat act ggg aaa ata ttt gcc | 390 |
| 83 | Phe Gln Val Arg Lys Val Thr Gly Ala Asn Thr Gly Lys Ile Phe Ala | |
| 84 | 110 115 120 | |
| 86 | atg aag gtg ctt aaa aag gca atg ata gta aga aat gct aaa gat aca | 438 |
| 87 | Met Lys Val Leu Lys Lys Ala Met Ile Val Arg Asn Ala Lys Asp Thr | |
| 88 | 125 130 135 | |
| 90 | gct cat aca aaa gca gaa cgg aat att ctg gag gaa gta aag cat ccc | 486 |
| 91 | Ala His Thr Lys Ala Glu Arg Asn Ile Leu Glu Glu Val Lys His Pro | |
| 92 | 140 145 150 | |
| 94 | ttc atc gtg gat tta att tat gcc ttt cag act ggt gga aaa ctc tac | 534 |
| 95 | Phe Ile Val Asp Leu Ile Tyr Ala Phe Gln Thr Gly Gly Lys Leu Tyr | |
| 96 | 155 160 165 | |
| 98 | ctc atc ctt gag tat ctc agt gga gga gaa cta ttt atg cag tta gaa | 582 |
| 99 | Leu Ile Leu Glu Tyr Leu Ser Gly Gly Glu Leu Phe Met Gln Leu Glu | |
| 100 | 170 175 180 185 | |
| 102 | aga gag gga ata ttt atg gaa gac act gcc tgc ttt tac ttg gca gaa | 630 |
| 103 | Arg Glu Gly Ile Phe Met Glu Asp Thr Ala Cys Phe Tyr Leu Ala Glu | |
| 104 | 190 195 200 | |
| 106 | atc tcc atg gct ttg ggg cat tta cat caa aag ggg atc atc tac aga | 678 |
| 107 | Ile Ser Met Ala Leu Gly His Leu His Gln Lys Gly Ile Ile Tyr Arg | |
| 108 | 205 210 215 | |
| 110 | gac ctg aag ccg gag aat atc atg ctt aat cac caa ggt cat gtg aaa | 726 |
| 111 | Asp Leu Lys Pro Glu Asn Ile Met Leu Asn His Gln Gly His Val Lys | |
| 112 | 220 225 230 | |
| 114 | cta aca gac ttt gga cta tgc aaa gaa tct att cat gat gga aca gtc | 774 |
| 115 | Leu Thr Asp Phe Gly Leu Cys Lys Glu Ser Ile His Asp Gly Thr Val | |
| 116 | 235 240 245 | |
| 118 | aca cac aca ttt tgt gga aca ata gaa tac atg gcc cct gaa atc ttg | 822 |
| 119 | Thr His Thr Phe Cys Gly Thr Ile Glu Tyr Met Ala Pro Glu Ile Leu | |
| 120 | 250 255 260 265 | |
| 122 | atg aga agt ggc cac aat cgt gct gtg gat tgg tgg agt ttg gga gca | 870 |
| 123 | Met Arg Ser Gly His Asn Arg Ala Val Asp Trp Trp Ser Leu Gly Ala | |
| 124 | 270 275 280 | |
| 126 | tta atg tat gac atg ctg act gga gca ccc cca ttc act ggg gag aat | 918 |
| 127 | Leu Met Tyr Asp Met Leu Thr Gly Ala Pro Pro Phe Thr Gly Glu Asn | |
| 128 | 285 290 295 | |
| 130 | aga aag aaa aca att gac aaa atc ctc aaa tgt aaa ctc aat ttg cct | 966 |
| 131 | Arg Lys Lys Thr Ile Asp Lys Ile Leu Lys Cys Lys Leu Asn Leu Pro | |
| 132 | 300 305 310 | |
| 134 | ccc tac ctc aca caa gaa gcc aga gat ctg ctt aaa aag ctg ctg aaa | 1014 |
| 135 | Pro Tyr Leu Thr Gln Glu Ala Arg Asp Leu Leu Lys Lys Leu Leu Lys | |
| 136 | 315 320 325 | |
| 138 | aga aat gct gct tct cgt ctg gga gct ggt cct ggg gac gct gga gaa | 1062 |

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139 Arg Asn Ala Ala Ser Arg Leu Gly Ala Gly Pro Gly Asp Ala Gly Glu
140 330                               335                               340                               345
142 gtt caa gct cat cca ttc ttt aga cac att aac tgg gaa gaa ctt ctg      1110
143 Val Gln Ala His Pro Phe Phe Arg His Ile Asn Trp Glu Glu Leu Leu
144                               350                               355                               360
146 gct cga aag gtg gag ccc ccc ttt aaa cct ctg ttg caa tct gaa gag      1158
147 Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser Glu Glu
148                               365                               370                               375
150 gat gta agt cag ttt gat tcc aag ttt aca cgt cag aca cct gtc gac      1206
151 Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro Val Asp
152                               380                               385                               390
154 agc cca gat gac tca act ctc agt gaa agt gcc aat cag gtc ttt ctg      1254
155 Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val Phe Leu
156                               395                               400                               405
158 ggt ttt aca tat gtg gct cca tct gta ctt gaa agt gtg aaa gaa aag      1302
159 Gly Phe Thr Tyr Val Ala Pro Ser Val Leu Glu Ser Val Lys Glu Lys
160 410                               415                               420                               425
162 ttt tcc ttt gaa cca aaa atc cga tca cct cga aga ttt att ggc agc      1350
163 Phe Ser Phe Glu Pro Lys Ile Arg Ser Pro Arg Arg Phe Ile Gly Ser
164                               430                               435                               440
166 cca cga aca cct gtc agc cca gtc aaa ttt tct cct ggg gat ttc tgg      1398
167 Pro Arg Thr Pro Val Ser Pro Val Lys Phe Ser Pro Gly Asp Phe Trp
168                               445                               450                               455
170 gga aga ggt gct tcg gcc agc aca gca aat cct cag aca cct gtg gaa      1446
171 Gly Arg Gly Ala Ser Ala Ser Thr Ala Asn Pro Gln Thr Pro Val Glu
172                               460                               465                               470
174 tac cca atg gaa aca agt ggc ata gag cag atg gat gtg aca atg agt      1494
175 Tyr Pro Met Glu Thr Ser Gly Ile Glu Gln Met Asp Val Thr Met Ser
176                               475                               480                               485
178 ggg gaa gca tcg gca cca ctt cca ata cga cag ccg aac tct ggg cca      1542
179 Gly Glu Ala Ser Ala Pro Leu Pro Ile Arg Gln Pro Asn Ser Gly Pro
180 490                               495                               500                               505
182 tac aaa aaa caa gct ttt ccc atg atc tcc aaa cgg cca gag cac ctg      1590
183 Tyr Lys Lys Gln Ala Phe Pro Met Ile Ser Lys Arg Pro Glu His Leu
184                               510                               515                               520
186 cgt atg aat cta tga cagagcaatg cttttaatga atttaaggca aaaaggtgga      1645
187 Arg Met Asn Leu
188                               525
190 gagggagatg tgtgagcatc ctgcaaggtg aaacaagact caaaatgaca gtttcagaga      1705
192 gtcaatgtca ttacatagaa cacttcggac acaggaaaaa taaacgtgga ttttaaaaaa      1765
194 tcaatcaatg gtgcaaaaaa aaacttaaag caaaatagta ttgctgaact cttaggcaca      1825
196 tcaattaatt gattcctcgc gacatctttc tcaaccttat caaggatttt catgttgatg      1885
198 actcgaaact gacagtatta agggtaggat gttgctctga atcactgtga gtctgatgtg      1945
200 tgaagaaggg tatcctttca ttaggcaagt acaaattgcc tataataactt gcaactaagg      2005
202 acaaattagc atgcaagctt ggtcaaactt ttcccaggca aaatgggaag gcaaagacaa      2065
204 aagaaactta ccaattgatg ttttacgtgc aaacaacctg aatctttttt ttatataaat      2125
206 atatattttt caaatagatt tttgattcag ctcatatga aaaacatccc aaactttaaa      2185
208 atgcgaaatt attggttggt gtgaagaaag ccagacaact tctgtttctt ctcttggtga      2245
210 aataataaaa tgcaaatgaa tcattgttaa cacagctgtg gctcgtttga gggattgggg      2305

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```

212 tggacctggg gtttattttc agtaaccacg ctgcggagcc t      2346
215 <210> SEQ ID NO: 4
216 <211> LENGTH: 24
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
222 <223> OTHER INFORMATION: PCR Primer
224 <400> SEQUENCE: 4
225 attgctgaac tcttaggcac atca      24
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 24
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: PCR Primer
237 <400> SEQUENCE: 5
238 tgtcagtttc gagtcatcaa catg      24
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 32
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
248 <223> OTHER INFORMATION: PCR Probe
250 <400> SEQUENCE: 6
251 ctgcgcacat ctttctcaac cttatcaagg at      32
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 19
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: PCR Primer
263 <400> SEQUENCE: 7
264 gaaggtgaag gtcggagtc      19
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 20
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
274 <223> OTHER INFORMATION: PCR Primer
276 <400> SEQUENCE: 8
277 gaagatggtg atgggatttc      20
280 <210> SEQ ID NO: 9
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
287 <223> OTHER INFORMATION: PCR Probe
289 <400> SEQUENCE: 9
290 caagcttccc gttctcagcc      20

```

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```

293 <210> SEQ ID NO: 10
294 <211> LENGTH: 20
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
300 <223> OTHER INFORMATION: Antisense Oligonucleotide
302 <400> SEQUENCE: 10
303 ggacccgccg cagcctcgtg 20
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 20
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
313 <223> OTHER INFORMATION: Antisense Oligonucleotide
315 <400> SEQUENCE: 11
316 tgggcccgga cccgccgcag 20
319 <210> SEQ ID NO: 12
320 <211> LENGTH: 20
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
326 <223> OTHER INFORMATION: Antisense Oligonucleotide
328 <400> SEQUENCE: 12
329 catgggcccgc gacccgccgc 20
332 <210> SEQ ID NO: 13
333 <211> LENGTH: 20
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
339 <223> OTHER INFORMATION: Antisense Oligonucleotide
341 <400> SEQUENCE: 13
342 ctcattgggcc cggacccgcc 20
345 <210> SEQ ID NO: 14
346 <211> LENGTH: 20
347 <212> TYPE: DNA
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
352 <223> OTHER INFORMATION: Antisense Oligonucleotide
354 <400> SEQUENCE: 14
355 gcctcatggg cccggacccg 20
358 <210> SEQ ID NO: 15
359 <211> LENGTH: 20
360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial Sequence
363 <220> FEATURE:
365 <223> OTHER INFORMATION: Antisense Oligonucleotide
367 <400> SEQUENCE: 15
368 tcgcctcatg ggcccggacc 20
371 <210> SEQ ID NO: 16

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/920,677

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date